

INFORMATION DISCLOSURE CITATION

Attorney Docket No.: GC626-3	Serial No.: 09/932,279
Applicant: Estell et al.	RECEIVED JAN 07 2003
Filing Date: August 17, 2001	
Page 2 of 2	Group: 1645 1631 Date of this Submission: January 3, 2002

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Examiner	Date Considered
<i>Andin Morales</i>	<i>1-9-04</i>

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PTO-1449

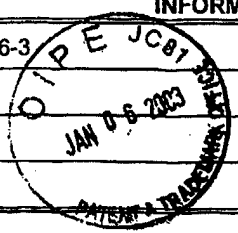
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Page 1 of 1	Date of this Submission: January 3, 2002

Examiner's	Document				Sub-	Translation
Initials	Number	Date	Country	Class	Class	Yes/No
AM	WO 00 20357 A	04/13/00	PCT			
AM	WO 97 37953 A	10/16/97	PCT			

Examiner's	
Initials	Author, Title, Date, Pertinent Pages, etc.
AM	Chen et al., "Isotope Edited Product Ion Assignment by alpha-N Labeling of peptides with ^3H (50%) β -Dinitrofluorobenzene," <i>J. of the American Society for Mass Spectrometry</i> , Elsevier Science, Inc., New York, NY, US, V. 10 (5), May 1999, pp. 448-452 Abstract
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Examiner	Date Considered
Audi Masoch	1-9-04
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Examiner's	
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	*Allen, G., "Sequencing of Proteins and Peptides," 2nd edn., Elsevier, Amsterdam, Book
AM	*Altschul et al., "Basic Local Alignment Search Tool," J. Mol. Biol., V. 215, 1990, pp. 403-410.
	*Bairoch et al., "The SWISS-PROT protein sequence database and its supplement TrEMBL in 2000," Nucl. Acids Res., Vol. 28, pp. 45-48, 2000.
	*Burks et al., "GeneBank: Current Status and Future Directions," Methods in Enzymology, V. 138, pp. 3-22 (1990).
	*Chowdhury et al., "Examination of Recombinant Truncated Mature Human Fibroblast Collagenase by Mass Spectrometry: Identification of Difference with the Published Sequence and Determination of Stable Isotope Incorporation," Rapid Commun. in Mass Spectrom., Vol. 9, pp. 563-569, 1995.
	*Corthals et al., "Identification of Proteins by Mass Spectrometry," Ed. Rabilloud, T. Springer, New York, pp. 197-231, 1999.
✓	*Christianson et al., "Peptide Mapping of Subtilisins as a Practical tool for Locating Protein Sequence Errors during Extensive Protein Engineering Projects," Anal. Biochem. 1994, Vol. 223, pp. 119-129.
	*Deutscher MP, "Guide to Protein purification," Academic Press, New York, Book
AM	*George et al., "PIR-International Protein Sequence Database", Methods in Enzymology, V. 266, pp. 41-59 (1996).
	*Goddette et al., "The Crystal Structure of the Bacillus lentus Alkaline Protease, Subtilisin BL, at 1.4 Å Resolution", J. Mol. Biol., V. 228, pp. 580-595 (1992).
	*Goeddel et al., "Synthesis of Human Fibroblast Interferon by E. coli," Nucl. Acids Res., Vol. 8, pp. 4057-4074, 1980.
	*Guermant et al., "Under Proper Control, Oxidation of Proteins with Known Chemical Structure Provides an Accurate and Absolute Method for the Determination of Their Molar Concentration", Anal. Biochem. V. 277, pp. 46-57 (2000).
✓	*Gygi et al., "Quantitative analysis of complex protein mixtures using isotope-coded affinity tags," Nature Biotech. V. 17, pp. 994-999 (1999).
	*Hale & Marham, The Harper Collins Dictionary of Biology, Harper Perennial, NY (1991) Book
	*Hancock ES, "New Methods in Peptide Mapping for the Characterization of Proteins", CRC Press, Boca Raton Book
AM	*Hsia et al., "Active-Site Titration of Serine Proteases Using a Fluoride Ion Selective Electrode and Sulfonyl Fluoride Inhibitors," Analytical Biochem., V. 242, pp. 221-227 (1996).
	*Janson et al., "Protein Purification," 2nd edn., Wiley-Liss, New York Book
	*Kellner et al., "Microcharacterization of Proteins", 2nd edn., Wiley-VCH, Weinheim Book
AM	*Khan et al., "EMBL Data Library", Methods in Enzymology, V. 183, pp. 23-31 (1990).
	Karlin et al., "Application and Statistics for Multiple High-Scoring Segments in Molecular Sequence," Proc. Natl. Acad. Sci. USA, V. 90, pp. 5873-5877 (1993).
✓	*Karlin et al., "Methods for assessing the statistical significance of molecular sequence features by using general scoring schemes," Proc. Natl. Acad. Sci. USA, V. 87, pp. 2264-2268 (1990).

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<i>John Manley</i>	<i>1-9-04</i>

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